O ¢eo

OIPE

```
                    RAW SEQUENCE LISTING            DATE: 11/09/2000
                    PATENT APPLICATION:  US/09/695,786    TIME: 11:59:10

                    Input Set : A:\CR9981 US DIV Seq Listing.txt
                    Output Set: N:\CRF3\11092000\I695786.raw
```

ENTERED

```
                    SEQUENCE LISTING
    3 (1) GENERAL INFORMATION:
    5      (i) APPLICANT: RAMESCH V. NAIR
    6                     MARK S. PAYNE
    7                     DONALD E. TRIMBUR
    8                     FERNANDO VALLE
   10     (ii) TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
   11                              GLYCEROL BY RECOMBINANT
   12                              ORGANISMS
   14    (iii) NUMBER OF SEQUENCES: 43
   16     (iv) CORRESPONDENCE ADDRESS:
   24          (A) ADDRESSEE: GENENCOR INTERNATIONAL, INC.
   25          (B) STREET: 4 CAMBRIDGE PLACE
   26                      1870 SOUTH WINTON ROAD
   27          (C) CITY: ROCHESTER
   28          (D) STATE: NEW YORK
   29          (E) COUNTRY: U.S.A.
   30          (F) ZIP: 14618
   32      (v) COMPUTER READABLE FORM:
   33          (A) MEDIUM TYPE: DISKETTE, 3.5 INCH
   34          (B) COMPUTER: IBM PC COMPATIBLE
   35          (C) OPERATING SYSTEM: MICROSOFT WINDOWS 95
   36          (D) SOFTWARE: MICROSOFT WORD VERSION 7.0A
   38     (vi) CURRENT APPLICATION DATA:
C--> 39          (A) APPLICATION NUMBER: US/09/695,786
C--> 40          (B) FILING DATE: 25-Oct-2000
   46          (C) CLASSIFICATION:
   43    (vii) PRIOR APPLICATION DATA:
   44          (A) APPLICATION NUMBER: 60/030602
   45          (B) FILING DATE: NOVEMBER 13, 1996
   48   (viii) ATTORNEY/AGENT INFORMATION:
   49          (A) NAME: FLOYD, LINDA AXAMETHY
   50          (B) REGISTRATION NUMBER: 33,692
   51          (C) REFERENCE/DOCKET NUMBER: CR-9981-B
   53     (ix) TELECOMMUNICATION INFORMATION:
   54          (A) TELEPHONE: 302-892-8112
   55          (B) TELEFAX: 302-773-0164
   58 (2) INFORMATION FOR SEQ ID NO: 1:
   60      (i) SEQUENCE CHARACTERISTICS:
   61          (A) LENGTH: 1380 base pairs
   62          (B) TYPE: nucleic acid
   63          (C) STRANDEDNESS: single
   64          (D) TOPOLOGY: linear
   66     (ii) MOLECULE TYPE: DNA (genomic)
C--> 68     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
   70 CTTTAATTTT CTTTTATCTT ACTCTCCTAC ATAAGACATC AAGAAACAAT TGTATATTGT    60
   72 ACACCCCCCC CCTCCACAAA CACAAATATT GATAATATAA AGATGTCTGC TGCTGCTGAT   120
```

```
RAW SEQUENCE LISTING                    DATE: 11/09/2000
PATENT APPLICATION:  US/09/695,786      TIME: 11:59:10

        Input Set : A:\CR9981 US DIV Seq Listing.txt
        Output Set: N:\CRF3\11092000\I695786.raw
```

```
 74 AGATTAAACT TAACTTCCGG CCACTTGAAT GCTGGTAGAA AGAGAAGTTC CTCTTCTGTT   180
 76 TCTTTGAAGG CTGCCGAAAA GCCTTTCAAG GTTACTGTGA TTGGATCTGG TAACTGGGGT   240
 78 ACTACTATTG CCAAGGTGGT TGCCGAAAAT TGTAAGGGAT ACCCAGAAGT TTTCGCTCCA   300
 80 ATAGTACAAA TGTGGGTGTT CGAAGAAGAG ATCAATGGTG AAAAATTGAC TGAAATCATA   360
 82 AATACTAGAC ATCAAAACGT GAAATACTTG CCTGGCATCA CTCTACCCGA CAATTTGGTT   420
 84 GCTAATCCAG ACTTGATTGA TTCAGTCAAG GATGTCGACA TCATCGTTTT CAACATTCCA   480
 86 CATCAATTTT TGCCCCGTAT CTGTAGCCAA TTGAAAGGTC ATGTTGATTC ACACGTCAGA   540
 88 GCTATCTCCT GTCTAAAGGG TTTTGAAGTT GGTGCTAAAG GTGTCCAATT GCTATCCTCT   600
 90 TACATCACTG AGGAACTAGG TATTCAATGT GGTGCTCTAT CTGGTGCTAA CATTGCCACC   660
 92 GAAGTCGCTC AAGAACACTG GTCTGAAACA ACAGTTGCTT ACCACATTCC AAACGATTTC   720
 94 AGAGGCGAGG GCAAGGACGT CGACCATAAG GTTCTAAAGG CCTTGTTCCA CAGACCTTAC   780
 96 TTCCACGTTA GTGTCATCGA AGATGTTGCT GGTATCTCCA TCTGTGGTGC TTTGAAGAAC   840
 98 GTTGTTGCCT TAGGTTGTGG TTTCGTCCAA GGTCTAGGCT GGGGTAACAA CGCTTCTGCT   900
100 GCCATCCAAA GAGTCGGTTT GGGTGAGATC ATCAGATTCG GTCAAATGTT TTTCCCAGAA   960
102 TCTAGAGAAG AAACATACTA CCAAGAGTCT GCTGGTGTTG CTGATTTGAT CACCACCTGC  1020
104 GCTGGTGGTA GAAACGTCAA GGTTGCTAGG CTAATGGCTA CTTCTGGTAA GGACGCCTGG  1080
106 GAATGTGAAA AGGAGTTGTT GAATGGCCAA TCCGCTCAAG GTTTAATTAC CTGCAAAGAA  1140
108 GTTCACGAAT GGTTGGAAAC ATGTGGCTCT GTCGAAGACT TCCCATTATT TGAAGCCGTA  1200
110 TACCAAATCG TTTACAACAA CTACCCAATG AAGAACCTGC CGGACATGAT TGAAGAATTA  1260
112 GATCTACATG AAGATTAGAT TTATTGGAGA AAGATAACAT ATCATACTTC CCCCACTTTT  1320
114 TTCGAGGCTC TTCTATATCA TATTCATAAA TTAGCATTAT GTCATTTCTC ATAACTACTT  1380
116 (2) INFORMATION FOR SEQ ID NO: 2:
118      (i) SEQUENCE CHARACTERISTICS:
119          (A) LENGTH: 2946 base pairs
120          (B) TYPE: nucleic acid
121          (C) STRANDEDNESS: single
122          (D) TOPOLOGY: linear
124      (ii) MOLECULE TYPE: DNA (genomic)
126      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
128 GAATTCGAGC CTGAAGTGCT GATTACCTTC AGGTAGACTT CATCTTGACC CATCAACCCC    60
130 AGCGTCAATC CTGCAAATAC ACCACCCAGC AGCACTAGGA TGATAGAGAT AATATAGTAC   120
132 GTGGTAACGC TTGCCTCATC ACCTACGCTA TGGCCGGAAT CGGCAACATC CCTAGAATTG   180
134 AGTACGTGTG ATCCGGATAA CAACGGCAGT GAATATATCT TCGGTATCGT AAAGATGTGA   240
136 TATAAGATGA TGTATACCCA ATGAGGAGCG CCTGATCGTG ACCTAGACCT TAGTGGCAAA   300
138 AACGACATAT CTATTATAGT GGGGAGAGTT TCGTGCAAAT AACAGACGCA GCAGCAAGTA   360
140 ACTGTGACGA TATCAACTCT TTTTTTATTA TGTAATAAGC AAACAAGCAC GAATGGGGAA   420
142 AGCCTATGTG CAATCACCAA GGTCGTCCCT TTTTTCCCAT TTGCTAATTT AGAATTTAAA   480
144 GAAACCAAAA GAATGAAGAA AGAAAACAAA TACTAGCCCT AACCCTGACT TCGTTTCTAT   540
146 GATAATACCC TGCTTTAATG AACGGTATGC CCTAGGGTAT ATCTCACTCT GTACGTTACA   600
148 AACTCCGGTT ATTTTATCGG AACATCCGAG CACCCGCGCC TTCCTCAACC CAGGCACCGC   660
150 CCCAGGTAAC CGTGCGCGAT GAGCTAATCC TGAGCCATCA CCCACCCCAC CCGTTGATGA   720
152 CAGCCAATTCG GGAGGGCGAA AATAAAACTG GAGCAAGGAA TTACCATCAC CGTCACCATC   780
154 ACCATCATAT CGCCTTAGCC TCTAGCCATA GCCATCATGC AAGCGTGTAT CTTCTAAGAT   840
156 TCAGTCATCA TCATTACCGA GTTTGTTTTC CTTCACATGA TGAAGAAGGT TTGAGTATGC   900
158 TCGAAACAAT AAGACGACGA TGGCTCTGCC ATTGGTTATA TTACGCTTTT GCGGCGAGGT   960
160 GCCGATGGGT TGCTGAGGGG AAGAGTGTTT AGCTTACGGA CCTATTGCCA TTGTTATTCC  1020
162 GATTAATCTA TTGTTCAGCA GCTCTTCTCT ACCCTGTCAT TCTAGTATTT TTTTTTTTTT  1080
164 TTTTTGGTTT TACTTTTTTT TCTTCTTGCC TTTTTTTCTT GTTACTTTTT TTCTAGTTTT  1140
166 TTTTCCTTCC ACTAAGCTTT TTCCTTGATT TATCCTTGGG TTCTTCTTTC TACTCCTTTA  1200
```

```
                    RAW SEQUENCE LISTING              DATE: 11/09/2000
                    PATENT APPLICATION: US/09/695,786  TIME: 11:59:11

                       Input Set : A:\CR9981 US DIV Seq Listing.txt
                       Output Set: N:\CRF3\11092000\I695786.raw

        168 GATTTTTTTT TTATATATTA ATTTTTAAGT TTATGTATTT TGGTAGATTC AATTCTCTTT  1260
        170 CCCTTTCCTT TTCCTTCGCT CCCCTTCCTT ATCAATGCTT GCTGTCAGAA GATTAACAAG  1320
        172 ATACACATTC CTTAAGCGAA CGCATCCGGT GTTATATACT CGTCGTGCAT ATAAAATTTT  1380
        174 GCCTTCAAGA TCTACTTTCC TAAGAAGATC ATTATTACAA ACACAACTGC ACTCAAAGAT  1440
        176 GACTGCTCAT ACTAATATCA AACAGCACAA ACACTGTCAT GAGGACCATC CTATCAGAAG  1500
        178 ATCGGACTCT GCCGTGTCAA TTGTACATTT GAAACGTGCG CCCTTCAAGG TTACAGTCAT  1560
        180 TGGTTCTGGT AACTGGGGGA CCACCATCGC CAAAGTCATT GCGGAAAACA CAGAATTGCA  1620
        182 TTCCCATATC TTCGAGCCAG AGGTGAGAAT GTGGGTTTTT GATGAAAAGA TCGGCGACGA  1680
        184 AAATCTGACG GATATCATAA ATACAAGACA CCAGAACGTT AAATATCTAC CCAATATTCA  1740
        186 CCTGCCCCAT AATCTAGTGG CCGATCCTGA TCTTTTACAC TCCATCAAGG GTGCTGACAT  1800
        188 CCTTGTTTTC AACATCCCTC ATCAATTTTT ACCAAACATA GTCAAACAAT TGCAAGGCCA  1860
        190 CGTGGCCCCT CATGTAAGGG CCATCTCGTG TCTAAAAGGG TTCGAGTTGG GCTCCAAGGG  1920
        192 TGTGCAATTG CTATCCTCCT ATGTTACTGA TGAGTTAGGA ATCCAATGTG GCGCACTATC  1980
        194 TGGTGCCAAAC TTGGCACCGG AAGTGGCCAA GGAGCATTGG TCCGAAACCA CCGTGGCTTA  2040
        196 CCAACTACCA AAGGATTATC AAGGTGATGG CAAGGATGTA GATCATAAGA TTTTGAAATT  2100
        198 GCTGTTCCAC AGACCTTACT TCCACGTCAA TGTCATCGAT GATGTTGCTG GTATATCCAT  2160
        200 TGCCGGTGCC TTGAAGAACG TCGTGGCACT TGCATGTGGT TTCGTAGAAG GTATGGGATG  2220
        202 GGGTAACAAT GCCTCCGCAG CCATTCAAAG GCTGGGTTTA GGTGAAATTA TCAAGTTCGG  2280
        204 TAGAATGTTT TTCCCAGAAT CCAAAGTCGA GACCTACTAT CAAGAATCCG CTGGTGTTGC  2340
        206 AGATCTGATC ACCACCTGCT CAGGCGGTAG AAACGTCAAG GTTGCCACAT ACATGGCCAA  2400
        208 GACCGGTAAG TCAGCCTTGG AAGCAGAAAA GGAATTGCTT AACGGTCAAT CCGCCCAAGG  2460
        210 GATAATCACA TGCAGAGAAG TTCACGAGTG GCTACAAACA TGTGAGTTGA CCCAAGAATT  2520
        212 CCCAATTATT CGAGGCAGTC TACCAGATAG TCTACAACAA CGTCCGCATG GAAGACCTAC  2580
        214 CGGAGATGAT TGAAGAGCTA GACATCGATG ACGAATAGAC ACTCTCCCCC CCCCTCCCCC  2640
        216 TCTGATCTTT CCTGTTGCCT CTTTTTCCCC CAACCAATTT ATCATTATAC ACAAGTTCTA  2700
        218 CAACTACTAC TAGTAACATT ACTACAGTTA TTATAATTTT CTATTCTCTT TTTCTTTAAG  2760
        220 AATCTATCAT TAACGTTAAT TTCTATATAT ACATAACTAC CATTATACAC GCTATTATCG  2820
        222 TTTACATATC ACATCACCGT TAATGAAAGA TACGACACCG TGTACACTAA CACAATTAAA  2880
        224 TAATCGCCAT AACCTTTTCT GTTATCTATA GCCCTTAAAG CTGTTTCTTC GAGCTTTTCA  2940
        226 CTGCAG                                                             2946
        228 (2) INFORMATION FOR SEQ ID NO: 3:
        230       (i) SEQUENCE CHARACTERISTICS:
        231           (A) LENGTH: 3178 base pairs
        232           (B) TYPE: nucleic acid
        233           (C) STRANDEDNESS: single
        234           (D) TOPOLOGY: linear
        236      (ii) MOLECULE TYPE: DNA (genomic)
C--> 238      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
        240 CTGCAGAACT TCGTCTGCTC TGTGCCCATC CTCGCGGTTA GAAAGAAGCT GAATTGTTTC    60
        242 ATGCGCAAGG GCATCAGCGA GTGACCAATA ATCACTGCAC TAATTCCTTT TTAGCAACAC   120
        244 ATACTTATAT ACAGCACCAG ACCTTATGTC TTTTCTCTGC TCCGATACGT TATCCCACCC   180
        246 AACTTTTATT TCAGTTTTGG CAGGGGAAAT TTCACAACCC CGCACGCTAA AAATCGTATT   240
        248 TAAACTTAAA AGAGAACAGC CACAAATAGG GAACTTTGGT CTAAACGAAG GACTCTCCCT   300
        250 CCCTTATCTT GACCGTGCTA TTGCCATCAC TGCTACAAGA CTAAATACGT ACTAATATAT   360
        252 GTTTTCGGTA ACGAGAAGAA GAGCTGCCGG TGCAGCTGCT GCCATGGCCA CAGCCACGGG   420
        254 GACGCTGTAC TGGATGACTA GCCAAGGTGA TAGGCCGTTA GTGCACAATG ACCCGAGCTA   480
        256 CATGGTGCAA TTCCCCACCG CCGCTCCACC GGCAGGTCTC TAGACCGAGAC CTCCTGGACC   540
        258 GTCTGCACAA GACGCATCAA TTCGACGTGT TGATCATCGG TGGCGGGGCC ACGGGGACAG   600
        260 GATGTGCCCT AGATGCTGCG ACCAGGGGAC TCAATGTGGC CCTTGTTGAA AAGGGGGATT   660
```

```
RAW SEQUENCE LISTING                    DATE: 11/09/2000
PATENT APPLICATION:  US/09/695,786      TIME: 11:59:11

    Input Set : A:\CR9981 US DIV Seq Listing.txt
    Output Set: N:\CRF3\11092000\I695786.raw

262 TTGCCTCGGG AACGTCGTCC AAATCTACCA AGATGATTCA CGGTGGGGTG CGGTACTTAG    720
264 AGAAGGCCTT CTGGGAGTTC TCCAAGGCAC AACTCGATCT GGTCATCGAG GCACTCAACG    780
266 AGCGTAAACA TCTTATCAAC ACTGCCCCTC ACCTGTGCAC GGTGCTACCA ATTCTGATCC    840
268 CCATCTACAG CACCTGGCAG GTCCCGTACA TCTATATGGG CTGTAAATTC TACGATTTCT    900
270 TTGGCGGTTC CCAAAACTTG AAAAAATCAT ACCTACTGTC CAAATCCGCC ACCGTGGACA    960
272 AGGCTCCCAT GCTTACCACA GACAATTTAA AGGCCTCGCT TGTGTACCAT GATGGGTCCT   1020
274 TTAACGACTC GCGTTTGAAC GCCACTTTAG CCATCACGGG TGTGGAGAAC GGCGCTACCG   1080
276 TCTTGATCTA TGTCGAGGTA CAAAAATTGA TCAAAGACCC AACTTCTGGT AAGGTTATCG   1140
278 GTGCCGAGGC CCGGGACGTT GAGACTAATG AGCTTGTCAG AATCAACGCT AAATGTGTGG   1200
280 TCAATGCCAC GGGCCCATAC AGTGACGCCA TTTTGCAAAT GGACCGCAAC CCATCCGGTC   1260
282 TGCCGGACTC CCCGCTAAAC GACAACTCCA AGATCAAGTC GACTTTCAAT CAAATCTCCG   1320
284 TCATGGACCC GAAAATGGTC ATCCCATCTA TTGGCGTTCA CATCGTATTG CCCTCTTTTT   1380
286 ACTCCCCGAA GGATATGGGT TTGTTGGACG TCAGAACCTC TGATGGCAGA GTGATGTTCT   1440
288 TTTTACCTTG GCACGGCAAA GTCCTTGCCG GCACCACGA CATCCCACTA AAGCAAGTCC    1500
290 CAGAAAACCC TATGCCTACA GAGGCTGATA TTCAAGATAT CTTGAAAGAA CTACAGCACT   1560
292 ATATCGAATT CCCCGTGAAA AGAGAAGACG TGCTAAGTGC ATGGGCTGGT GTCAGACCTT   1620
294 TGGTCAGAGA TCCACGTACA ATCCCCGCAG ACGGGGAAGAA GGGCTCTGCC ACTCAGGGCG   1680
296 TGGTAAGATC CCACTTCTTG TTCACTTCGG ATAATGGCCT AATTACTATT GCAGGTGGTA   1740
298 AATGGACTAC TTACAGACAA ATGGCTGAGG AAACAGTCGA CAAAGTTGTC GAAGTTGGCG   1800
300 GATTCCACAA CCTGAAACCT TGTCACACAA GAGATATTAA GCTTGCTGGT GCAGAAGAAT   1860
302 GGACGCAAAA CTATGTGGCT TTATTGGCTC AAAACTACCA TTTATCATCA AAAATGTCCA   1920
304 ACTACTTGGT TCAAAACTAC GGAACCCGTT CCTCTATCAT TTGCGAATTT TTCAAAGAAT   1980
306 CCATGGAAAA TAAACTGCCT TTGTCCTTAG CCGACAAGGA AAATAACGTA ATCTACTCTA   2040
308 GCGAGGAGAA CAACTTGGTC AATTTTGATA CTTTCAGATA TCCATTCACA ATCGGTGAGT   2100
310 TAAAGTATTC CATGCAGTAC GAATATTGTA GAACTCCCTT GGACTTCCTT TTAAGAAGAA   2160
312 CAAGATTCGC CTTCTTGGAC GCCAAGGAAG CTTTGAATGC CGTGCATGCC ACCGTCAAAG   2220
314 TTATGGGTGA TGAGTTCAAT TGGTCGGAGA AAAAGAGGCA GTGGGAACTT GAAAAAACTG   2280
316 TGAACTTCAT CCAAGGACGT TTCGGTGTCT AAATCGATCA TGATAGTTAA GGGTGACAAA   2340
318 GATAACATTC ACAAGAGTAA TAATAATGGT AATGATGATA ATAATAATAA TGATAGTAAT   2400
320 AACAATAATA ATAATGGTGG TAATGGCAAT GAAATCGCTA TTATTACCTA TTTTTCCTTAA   2460
322 TGGAAGAGTT AAAGTAAACT AAAAAAACTA CAAAAATATA TGAAGAAAAA AAAAAAAAGA   2520
324 GGTAATAGAC TCTACTACTA CAATTGATCT TCAAATTATG ACCTTCCTAG TGTTTATATT   2580
326 CTATTTCCAA TACATAATAT AATCTATATA ATCATTGCTG GTAGACTTCC GTTTTAATAT   2640
328 CGTTTTAATT ATCCCCTTTA TCTCTAGTCT AGTTTTATCA TAAAATATAG AAACACTAAA   2700
330 TAATATTCTT CAAACGGTCC TGGTGCATAC GCAATACATA TTTATGGTGC AAAAAAAAAA   2760
332 ATGGAAAATT TTGCTAGTCA TAAACCCTTT CATAAAACAA TACGTAGACA TCGCTACTTG   2820
334 AAATTTTCAA GTTTTTATCA GATCCATGTT TCCTATCTGC CTTGACAACC TCATCGTCGA   2880
336 AATAGTACCA TTTAGAACGC CCAATATTCA CATTGTGTTC AAGGTCTTTA TTCACCAGTG   2940
338 ACGTGTAATG GCCATGATTA ATGTGCCTGT ATGGTTAACC ACTCCAAATA GCTTATATTT   3000
340 CATAGTGTCA TTGTTTTTCA ATATAATGTT TAGTATCAAT GGATATGTTA CGACGGTGTT   3060
342 ATTTTTCTTG GTCAAATCGT AATAAAATCT CGATAAATGG ATGACTAAGA TTTTTGGTAA   3120
344 ACTTACAAAA TTTATCGTTT TCACTGTTGT CAATTTTTTG TTCTTGTAAT CACTCCAG     3178
346 (2) INFORMATION FOR SEQ ID NO: 4:
348      (i) SEQUENCE CHARACTERISTICS:
349          (A) LENGTH: 816 base pairs
350          (B) TYPE: nucleic acid
351          (C) STRANDEDNESS: single
352          (D) TOPOLOGY: linear
354      (ii) MOLECULE TYPE: DNA (genomic)
```

```
C--> 356     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
     358 ATGAAACGTT TCAATGTTTT AAAATATATC AGAACAACAA AAGCAAATAT ACAAACCATC     60
     360 GCAATGCCTT TGACCACAAA ACCTTTATCT TTGAAAATCA ACGCCGCTCT ATTCGATGTT    120
     362 GACGGTACCA TCATCATCTC TCAACCAGCC ATTGCTGCTT TCTGGAGAGA TTTCGGTAAA    180
     364 GACAAGCCTT ACTTCGATGC CGAACACGTT ATTCACATCT CTCACGGTTG GAGAACTTAC    240
     366 GATCCCATTG CCAAGTTCGC TCCAGACTTT GCTGATGAAG AATACGTTAA CAACCTAGAA    300
     368 GGTGAAATCC CAGAAAAGTA CGGTGAACAC TCCATCGAAG TTCCAGGTGC TGTCAAGTTG    360
     370 TGTAATGCTT TGAACGCCTT GCCAAAGGAA AAATGGGCTG TCGCCACCTC TGGTACCCGT    420
     372 GACATGGCCA AGAAATGGTT CGACATTTTG AAGATCAAGA GACCAGAATA CTTCATCACC    480
     374 GCCAATGATG TCAAGCAAGG TAAGCCTCAC CCAGAACCAT ACTTAAAGGG TAGAAACGGT    540
     376 TTGGGTTTCC CAATTAATGA ACAAGACCCA TCCAAATCTA AGGTTGTTGT CTTTCAAGAC    600
     378 GCACCAGCTG GTATTGCTGC TGGTAAGGCT GCTGGCTGTA AAATCGTTGG TATTGCTACC    660
     380 ACTTTCGATT TGGACTTCTT GAAGGAAAAG GGTTGTGACA TCATTGTCAA GAACCACGAA    720
     382 TCTATCAGAC TCGGTGAATA CAACGCTGAA ACCGATGAAG TCGAATTGAT CTTTGATGAC    780
     384 TACTTATACG CTAAGGATGA CTTGTTGAAA TGGTAA                              816
     386 (2) INFORMATION FOR SEQ ID NO: 5:
     388      (i) SEQUENCE CHARACTERISTICS:
     389           (A) LENGTH: 753 base pairs
     390           (B) TYPE: nucleic acid
     391           (C) STRANDEDNESS: single
     392           (D) TOPOLOGY: linear
     394     (ii) MOLECULE TYPE: DNA (genomic)
C--> 396  .  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
     398 ATGGGATTGA CTACTAAACC TCTATCTTTG AAAGTTAACG CCGCTTTGTT CGACGTCGAC     60
     400 GGTACCATTA TCATCTCTCA ACCAGCCATT GCTGCATTCT GGAGGGATTT CGGTAAGGAC    120
     402 AAACCTTATT TCGATGCTGA ACACGTTATC CAAGTCTCGC ATGGTTGGAG AACGTTTGAT    180
     404 GCCATTGCTA AGTTCGCTCC ACACTTTGCC AATGAAGAGT ATGTTAACAA ATTAGAAGCT    240
     406 GAAATTCCGG TCAAGTACGG TGAAAAATCC ATTGAAGTCC CAGGTGCAGT TAAGCTGTGC    300
     408 AACGCTTTGA ACGCTCTACC AAAAGAGAAA TGGGCTGTGG CAACTTCCGG TACCCGTGAT    360
     410 ATGGCACAAA AATGGTTCGA GCATCTGGGA ATCAGGAGAC CAAAGTACTT CATTACCGCT    420
     412 AATGATGTCA AACAGGGTAA GCCTCATCCA GAACCATATC TGAAGGGCAG GAATGGCTTA    480
     414 GGATATCCGA TCAATGAGCA AGACCCTTCC AAATCTAAGG TAGTAGTATT TGAAGACGCT    540
     416 CCAGCAGGTA TTGCCGCCGG AAAAGCCGCC GGTTGTAAGA TCATTGGTAT TGCCACTACT    600
     418 TTCGACTTGG ACTTCCTAAA GGAAAAAGGC TGTGACATCA TTGTCAAAAA CCACGAATCC    660
     420 ATCAGAGTTG GCGGCTACAA TGCCGAAACA GACGAAGTTG AATTCATTTT TGACGACTAC    720
     422 TTATATGCTA AGGACGATCT GTTGAAATGG TAA                                 753
     424 (2) INFORMATION FOR SEQ ID NO: 6:
     426      (i) SEQUENCE CHARACTERISTICS:
     427           (A) LENGTH: 2520 base pairs
     428           (B) TYPE: nucleic acid
     429           (C) STRANDEDNESS: single
     430           (D) TOPOLOGY: linear
     432     (ii) MOLECULE TYPE: DNA (genomic)
C--> 434     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
     436 TGTATTGGCC ACGATAACCA CCCTTTGTAT ACTGTTTTTG TTTTTCACAT GGTAAATAAC     60
     438 GACTTTTATT AAACAACGTA TGTAAAAACA TAACAAGAAT CTACCCATAC AGGCCATTTC    120
     440 GTAATTCTTC TCTTCTAATT GGAGTAAAAC CATCAATTAA AGGGTGTGGA GTAGCATAGT    180
     442 GAGGGGCTGA CTGCATTGAC AAAAAAATTG AAAAAAAAAA AGGAAAAGGA AAGGAAAAAA    240
     444 AGACAGCCAA GACTTTTAGA ACGGATAAGG TGTAATAAAA TGTGGGGGGA TGCCTGTTCT    300
```

VERIFICATION SUMMARY   DATE: 11/09/2000
PATENT APPLICATION: US/09/695,786   TIME: 11:59:12

Input Set : A:\CR9981 US DIV Seq Listing.txt
Output Set: N:\CRF3\11092000\I695786.raw

```
L:39 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:40 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:68 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:126 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:238 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:356 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:396 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:434 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:530 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:617 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:701 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:830 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:907 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1015 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1129 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1189 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1252 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1399 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1413 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1427 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1441 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1455 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1469 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1483 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1497 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1516 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1535 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1550 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1565 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1580 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1595 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1610 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1625 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1640 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1655 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1670 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1685 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1700 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1715 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1730 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1745 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1760 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1775 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1790 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1805 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
```